

SEQUENCE LISTING

<110> NOVIMMUNE SA c/o MEDABIOTECH SA

<120> NEW TRANSCRIPTION FACTOR OF MHC CLASS II GENES,
SUBSTANCES CAPABLE OF INHIBITING THIS NEW TRANSCRIPTION
FACTOR AND MEDICAL USES OF THESE SUBSTANCES

<130> B3991A-GD/LL

<140> PCT/EP

<141> 1999-10-22

<150> 98120085.0

<151> 1998-10-24

<160> 19

<170> PatentIn Ver. 2.1

<210> 1

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 1

ccgtacgcgt ctagaccatg gagcttacct agcctgcaga

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<210> 2

<211> 31

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:primer

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ttcgaattct cgagtgtctg agtccccggc a

31

<210> 3

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:primer

<400> 3

ccgtacgcgt ctagaccatg gagcccactc aggttgc

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:primer

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ttcgaattct cgagtgcctg gggtccagca gg

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<210> 5

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ccagctctag actccaccac tctcaccaac

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<212> DNA

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<223> Description of Artificial Sequence:primer

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<210> 7

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<212> DNA

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<223> Description of Artificial Sequence:primer

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ggttctctag attggcagca ctggggatag

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<210> 8

<211> 30

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:primer

<400> 8

gctacgaatt ccagcagaca cagccaaaac

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<210> 9

<211> 69

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:primer

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ccgtacgcgt ctagaatgga ttacaaagac gatgacgata agatggagct tacccagcct 60

gcagaagac

69

<210> 10

<211> 1345

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (418)..(1200)

<400> 10

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ggctggtgga gcgacacca ggcaggagag ggggaagaac tctctccctt tctgaacccc 120

cttttccttg agagacgagt tgggggagtc ctccacgcat taccactcg ggccgcaaaa																180
actcccttct ttagccctct gcccccgccc ttgcttataa gcctttgaga ccgcagaagg																240
gaccttggtg tggaacggga cggccaagag gaagccagat cgctgagggg ccggtctcca																300
gtttgcctcc tgctatatcc attggaagag aaaagtttgt gacttggggc cccaagtttt																360
gagagaactg ggctttcggc gcgggggggac agaggaggct cgtgggggagc tttcccc																417
atg gag ctt acc cag cct gca gaa gac ctc atc cag acc cag cag acc																465
Met	Glu	Leu	Thr	Gln	Pro	Ala	Glu	Asp	Leu	Ile	Gln	Thr	Gln	Gln	Thr	
1				5					10				15			
cct gcc tca gaa ctt ggg gac cct gaa gac ccc gga gag gag gct gca																513
Pro	Ala	Ser	Glu	Leu	Gly	Asp	Pro	Glu	Asp	Pro	Gly	Glu	Glu	Ala	Ala	
			20					25				30				
gat ggc tca gac act gtg gtc ctc agt ctc ttt ccc tgc acc cct gag																561
Asp	Gly	Ser	Asp	Thr	Val	Val	Leu	Ser	Leu	Phe	Pro	Cys	Thr	Pro	Glu	
		35					40					45				
cct gtg aat cct gaa ccg gat gcc agt gtt tcc tct cca cag gca ggc																609
Pro	Val	Asn	Pro	Glu	Pro	Asp	Ala	Ser	Val	Ser	Ser	Pro	Gln	Ala	Gly	
	50					55					60					
agc tcc ctg aag cac tcc acc act ctc acc aac cgg cag cga ggg aac																657
Ser	Ser	Leu	Lys	His	Ser	Thr	Thr	Leu	Thr	Asn	Arg	Gln	Arg	Gly	Asn	
65					70					75				80		
gag gtg tca gct ctg ccg gcc acc cta gac tcc ctg tcc atc cac cag																705
Glu	Val	Ser	Ala	Leu	Pro	Ala	Thr	Leu	Asp	Ser	Leu	Ser	Ile	His	Gln	
				85				90					95			
ctc gca gca cag ggg gag ctg gac cag ctg aag gag cat ttg cgg aaa																753
Leu	Ala	Ala	Gln	Gly	Glu	Leu	Asp	Gln	Leu	Lys	Glu	His	Leu	Arg	Lys	
			100				105					110				
ggg gac aac ctc gtc aac aag cca gac gag cgc ggc ttc acc ccc ctc																801
Gly	Asp	Asn	Leu	Val	Asn	Lys	Pro	Asp	Glu	Arg	Gly	Phe	Thr	Pro	Leu	
		115				120					125					
atc tgg gcc tcc gcc ttt gga gag att gag acc gtt cgc ttc ctg ctg																849
Ile	Trp	Ala	Ser	Ala	Phe	Gly	Glu	Ile	Glu	Thr	Val	Arg	Phe	Leu	Leu	
	130					135					140					
gag tgg ggt gcc gac ccc cac atc ctg gca aaa gag cga gag agc gcc																897
Glu	Trp	Gly	Ala	Asp	Pro	His	Ile	Leu	Ala	Lys	Glu	Arg	Glu	Ser	Ala	

Asp Gly Ser Asp Thr Val Val Leu Ser Leu Phe Pro Cys Thr Pro Glu

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Pro Val Asn Pro Glu Pro Asp Ala Ser Val Ser Ser Pro Gln Ala Gly
50 55 60

Ser Ser Leu Lys His Ser Thr Thr Leu Thr Asn Arg Gln Arg Gly Asn
65 70 75 80

Glu Val Ser Ala Leu Pro Ala Thr Leu Asp Ser Leu Ser Ile His Gln
85 90 95

Leu Ala Ala Gln Gly Glu Leu Asp Gln Leu Lys Glu His Leu Arg Lys
100 105 110

Gly Asp Asn Leu Val Asn Lys Pro Asp Glu Arg Gly Phe Thr Pro Leu
115 120 125

Ile Trp Ala Ser Ala Phe Gly Glu Ile Glu Thr Val Arg Phe Leu Leu
130 135 140

Glu Trp Gly Ala Asp Pro His Ile Leu Ala Lys Glu Arg Glu Ser Ala
145 150 155 160

Leu Ser Leu Ala Ser Thr Gly Gly Tyr Thr Asp Ile Val Gly Leu Leu
165 170 175

Leu Glu Arg Asp Val Asp Ile Asn Ile Tyr Asp Trp Asn Gly Gly Thr
180 185 190

Pro Leu Leu Tyr Ala Val Arg Gly Asn His Val Lys Cys Val Glu Ala
195 200 205

Leu Leu Ala Arg Gly Ala Asp Leu Thr Thr Glu Ala Asp Ser Gly Tyr
210 215 220

Thr Pro Met Asp Leu Ala Val Ala Leu Gly Tyr Arg Lys Val Gln Gln
225 230 235 240

Val Ile Glu Asn His Ile Leu Lys Leu Phe Gln Ser Asn Leu Val Pro
245 250 255

Ala Asp Pro Glu
260

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<400> 12
Met Glu Leu Thr Gln Pro Ala Glu Asp Leu Ile Gln Thr Gln Gln Thr
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Pro Ala Ser Glu Leu Gly Asp Pro Glu Asp Pro Gly Glu Glu Ala Ala
      20              25              30

Asp Gly Ser Asp Thr Val Val Leu Ser Leu Phe Pro Cys Thr Pro Glu
      35              40              45

Pro Val Asn Pro Glu Pro Asp Ala Ser Val Ser Ser Pro Gln Ala Gly
      50              55              60

Ser Ser Leu Lys His Ser Thr Thr Leu Thr Asn Arg Gln Arg Gly Asn
  65              70              75              80

Glu Val Ser Ala Leu Pro Ala Thr Leu Asp Ser Leu Ser Ile His Gln
      85              90              95

Leu Ala Ala Gln Gly Glu Leu Asp Gln Leu Lys Glu His Leu Arg Lys
      100             105             110

Gly Asp Asn Leu Val Asn Lys Pro Asp Glu Arg Gly Phe Thr Pro Leu
      115             120             125

Ile Trp Ala Ser Ala Phe Gly Glu Ile Glu Thr Val Arg Phe Leu Leu
  130             135             140

Glu Trp Gly Ala Asp Pro His Ile Leu Ala Lys Glu Arg Glu Ser Ala
  145             150             155             160

Leu Ser Leu Ala Ser Thr Gly Gly Tyr Thr Asp Ile Val Gly Leu Leu
      165             170             175

Leu Glu Arg Asp Val Asp Ile Asn Ile Tyr Asp Trp Asn Gly Gly Thr
      180             185             190

Pro Leu Leu Tyr Ala Val Arg Gly Asn His Val Lys Cys Val Glu Ala
      195             200             205

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Leu Leu Ala Arg Gly Ala Asp Leu Thr Thr Glu Ala Asp Ser Gly Tyr
 210 215 220

Thr Pro Met Asp Leu Ala Val Ala Leu Gly Tyr Arg Lys Val Gln Gln
 225 230 235 240

Val Ile Glu Asn His Ile Leu Lys Leu Phe Gln Ser Asn Leu Val Pro
 245 250 255

Ala Asp Pro Glu
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<210> 13

<211> 269

<212> PRT

<213> Murinae gen. sp.

<400> 13

Met Glu Pro Thr Gln Val Ala Glu Asn Leu Val Pro Asn Gln Gln Pro
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Pro Val Pro Asp Leu Glu Asp Pro Glu Asp Thr Arg Asp Glu Ser Pro
 20 25 30

Glu Asn Ser Asp Thr Val Val Leu Ser Leu Phe Pro Cys Thr Pro Asp
 35 40 45

Ala Val Asn Pro Glu Ala Asp Ala Ser Ala Ser Ser Leu Gln Gly Ser
 50 55 60

Phe Leu Lys His Ser Thr Thr Leu Thr Asn Arg Gln Arg Gly Asn Glu
 65 70 75 80

Val Ser Ala Leu Pro Ala Thr Leu Asp Ser Leu Ser Ile His Gln Leu
 85 90 95

Ala Ala Gln Gly Glu Leu Ser Gln Leu Lys Asp His Leu Arg Lys Gly
 100 105 110

Ala Cys Pro Ala Cys Thr Cys Leu Ser Gly Asn Asn Leu Ile Asn Lys
 115 120 125

Pro Asp Glu Arg Gly Phe Thr Pro Leu Ile Trp Ala Ser Ala Phe Gly
 130 135 140

Glu Ile Glu Thr Val Arg Phe Leu Leu Asp Trp Gly Ala Asp Pro His
 145 150 155 160

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<400> 18

Asn Ala Phe Asn Val Phe Thr Phe Val Phe His Leu Ala Glu Cys Asn
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Ile His Thr Ser Pro Ser Pro Gly Ile Gln Val Arg His Val Xaa Thr
20 25 30

Pro Ser Thr Thr Lys His Phe Ser Pro Ile Lys Gln Ser Thr Thr Leu
35 40 45

Thr Asn Lys His Arg Gly Asn Glu Val Ser Thr Thr Pro Leu Leu Ala
50 55 60

Asn Ser Leu Ser Val His Gln Leu Ala Ala Gln Gly Glu Met Leu Tyr
65 70 75 80

Leu Ala Thr Arg Ile Glu Gln Glu Asn Val Ile Asn His Thr Asp Glu
85 90 95

Glu Gly Phe Thr Pro Leu Met Trp Ala Ala Ala His Gly Gln Ile Ala
100 105 110

Val Val Glu Phe Leu Leu Gln Asn Gly Ala Asp Pro Gln Leu Leu Gly
115 120 125

Lys Gly Arg Glu Ser Ala Leu Ser Leu Ala Cys Ser Lys Gly Tyr Thr
130 135 140

Asp Ile Val Xaa Met Leu Leu Asp Cys Gly Val Asp Val Asn Xaa Tyr
145 150 155 160

Asp Trp Asn Gly Gly Thr Pro Leu Leu Tyr Ala Val His Gly Asn His
165 170 175

Val Lys Cys Val Lys Met Leu Leu Glu Ser Gly Ala Asp Pro Thr Ile
180 185 190

Glu Thr Asp Ser Gly Tyr Asn Ser Met Asp Leu Ala Val Ala Leu Gly
195 200 205

Ile Glu Val Phe Asn Arg Leu Leu Ser His Ile Cys
210 215 220

<210> 19

<211> 218

<212> PRT

<213> Murinae gen. sp.

<400> 19

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Ala Ser Val Leu Phe Lys Ala Glu Cys Asn Ile His Thr Ser Pro Ser
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Pro Gly Ile Gln Val Arg His Val Tyr Thr Pro Ser Thr Thr Lys His
20 25 30

Phe Ser Pro Ile Lys Gln Ser Thr Thr Leu Thr Asn Lys His Arg Gly
35 40 45

Asn Glu Val Ser Thr Thr Pro Leu Leu Ala Asn Ser Leu Ser Ala His
50 55 60

Gln Leu Ala Ala Gln Gly Glu Met Leu Tyr Leu Ala Thr Arg Ile Glu
65 70 75 80

Gln Glu Asn Val Ile Asn His Thr Asp Glu Glu Gly Phe Thr Pro Leu
85 90 95

Met Trp Ala Ala Ala His Gly Gln Ile Ala Val Val Glu Phe Leu Leu
100 105 110

Gln Asn Gly Ala Asp Pro Gln Leu Leu Gly Lys Gly Arg Glu Ser Ala
115 120 125

Leu Ser Leu Ala Cys Ser Lys Gly Tyr Thr Asp Ile Val Lys Met Leu
130 135 140

Leu Asp Cys Gly Val Asp Val Asn Glu Tyr Asp Trp Asn Gly Gly Thr
145 150 155 160

Pro Leu Leu Tyr Ala Gly His Gly Asn His Val Lys Cys Val Lys Met
165 170 175

Leu Leu Glu Asn Gly Ala Asp Pro Thr Ile Glu Thr Asp Ser Gly Tyr
180 185 190

Asn Ser Met Asp Leu Ala Val Ala Leu Gly Ile Glu Gly Cys Ser Asp
195 200 205

Tyr Met Leu Val Thr Asp Val Phe Arg Ile
210 215